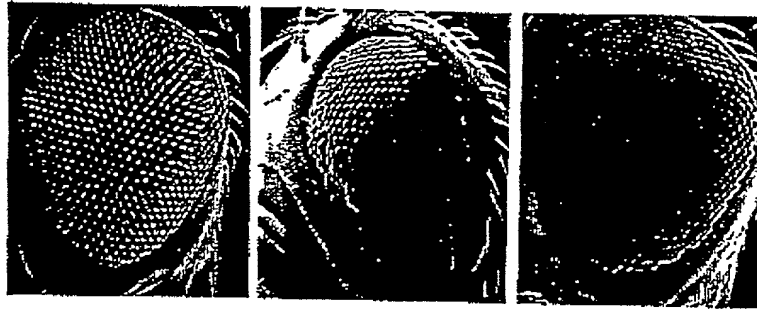


Figure 1

A



wild type

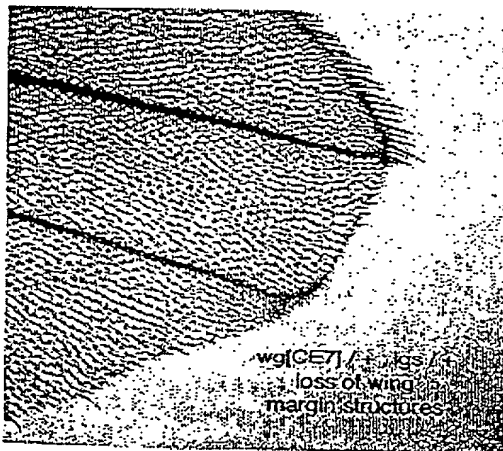
sev-wg

sev-wg, lgs<sup>S17</sup>/+

B



C



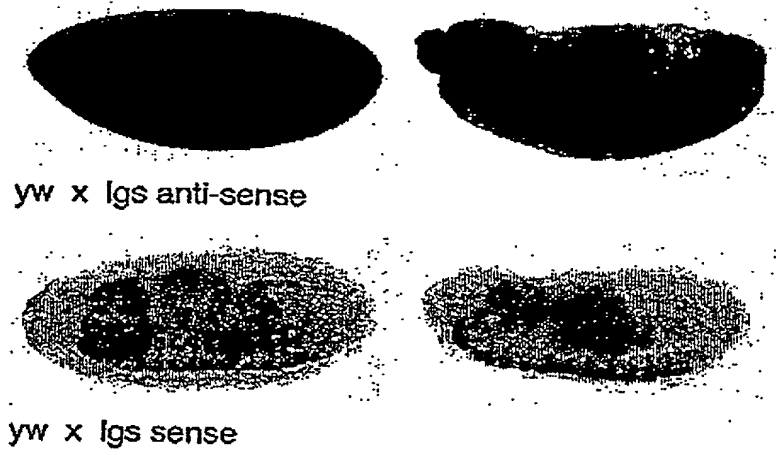
009454-020  
 10/22/00 07:55:660

[illegible][illegible]

AAAAAAAAAA 6909

Figure 3

A



B

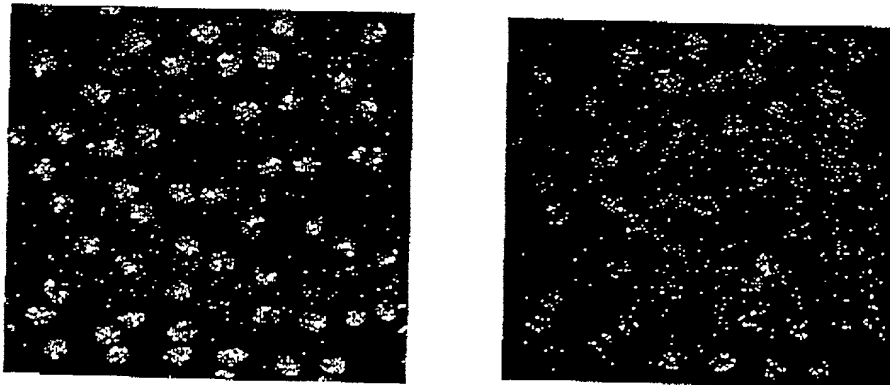
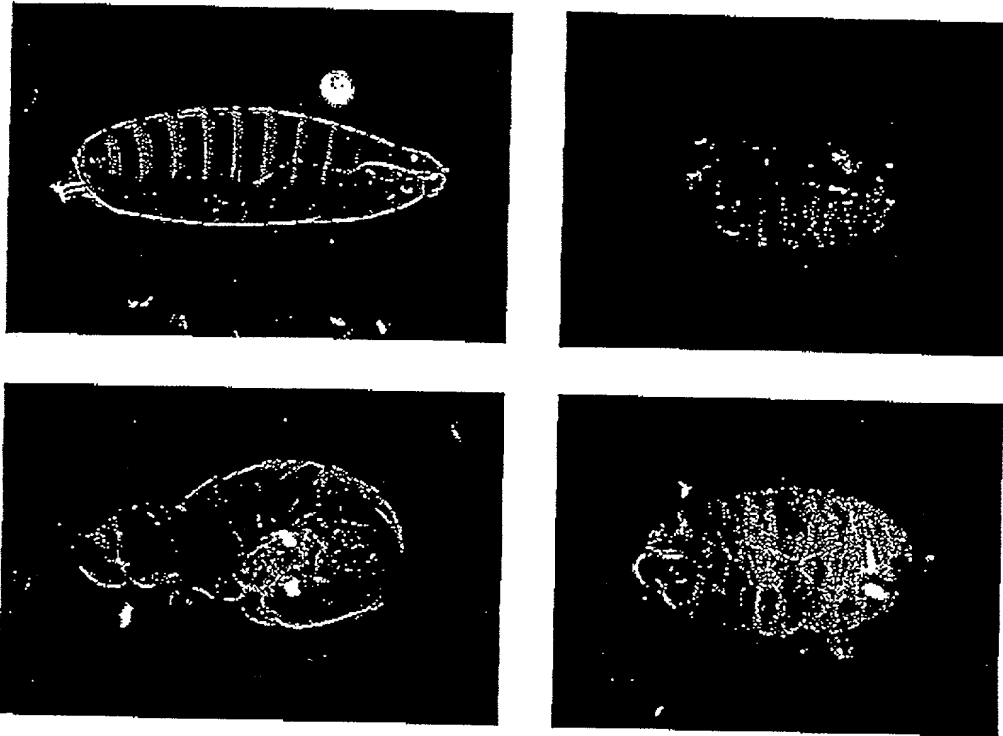


Figure 4



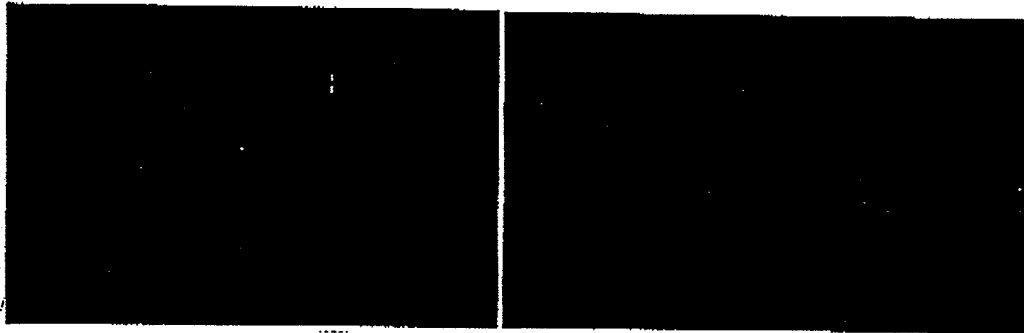
Q-60361

Figure 5

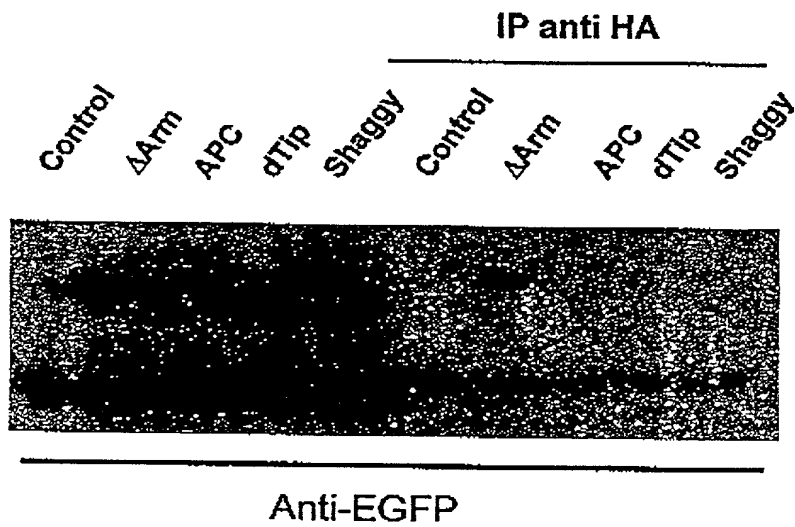
A

EGFP-Lgs

EGFP-Lgs + pcDNA3-Arm-NLS



B

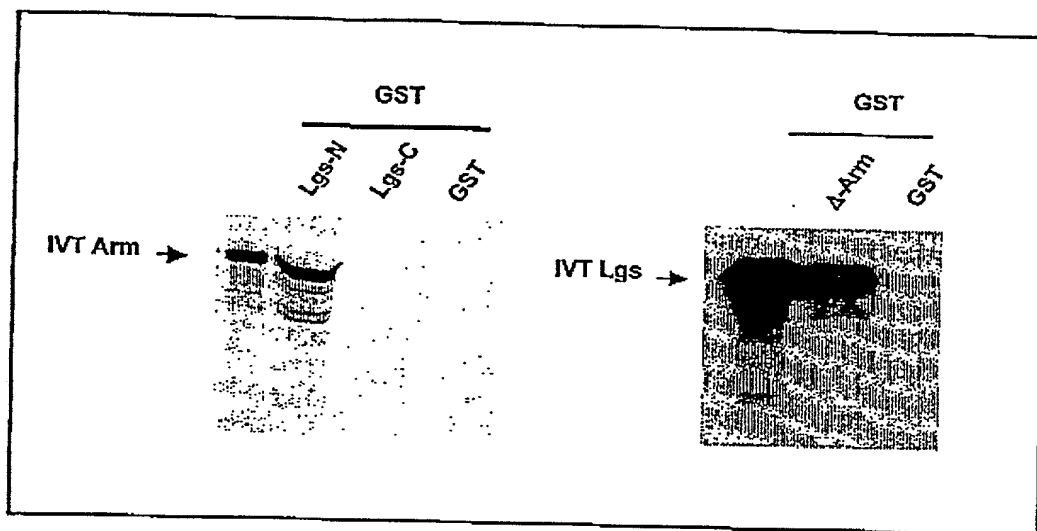


5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	$\Delta$ ArmC	$\Delta$ $\beta$ -Cat	Pan
PREY fusions: pJG4-5	lgs364-555							
	lgs1-385							
	lgs1-732							
	lgs364-1090							
	lgs726-1464							
	lgs1-1464							
	BCL9 199-392							
	BCL91-1426							
	Dco+							
	DAXin							
	$\Delta$ ArmC							
	$\beta$ -Cat							
	Pan							
	pJG4-5							

+: interaction seen in yeast two-hybrid assay  
 -: no interaction seen in yeast two-hybrid assay  
 n.d.: not done  
 numberings refer to amino acid positions.

5D



5E

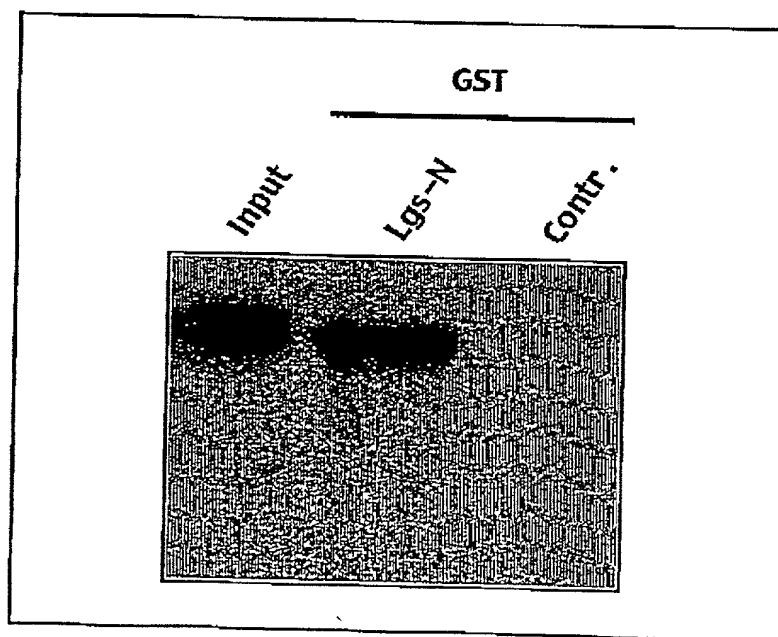




Figure 6

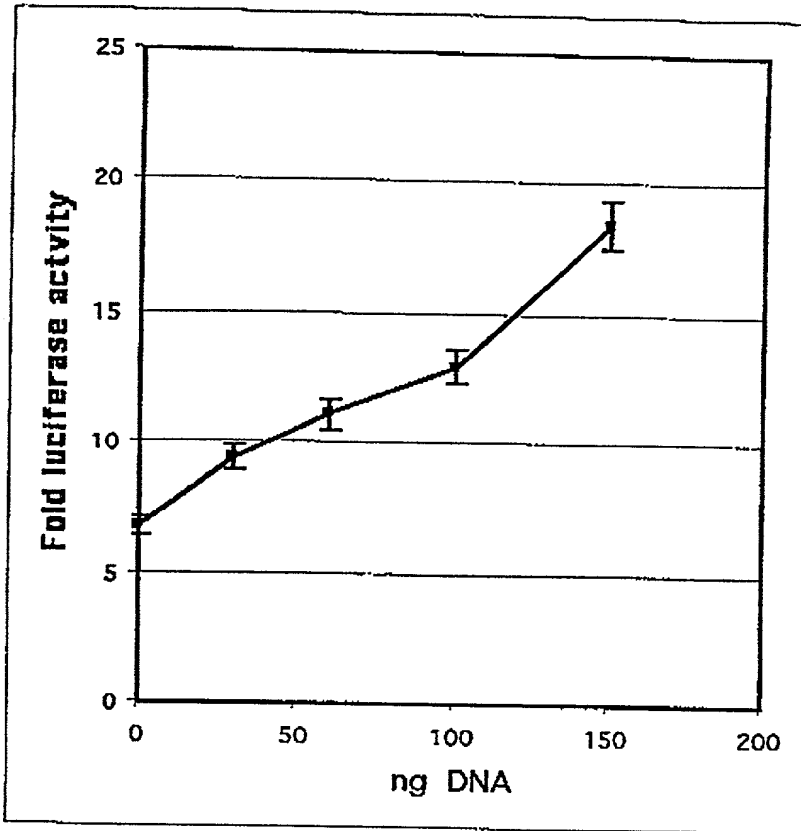
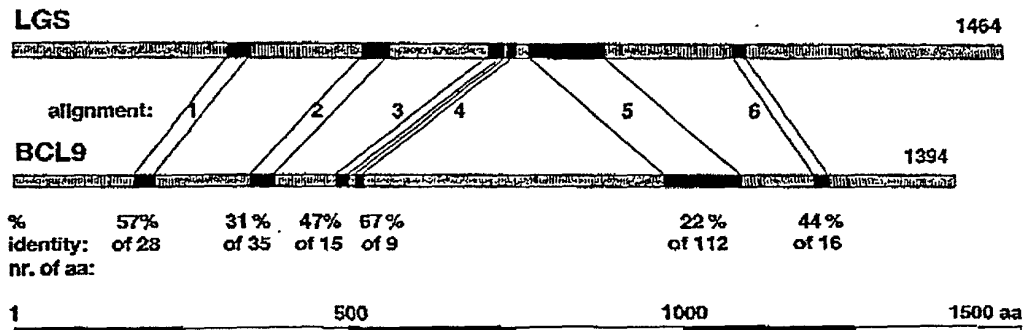


Figure 7

A



bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted March 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

**Sequence homology domain 1: 57.1% identity in 28 aa**

**Sequence homology domain 2: 31.4% identity in 35 aa**

**Sequence homology domain 3: 46.7% identity in 15 aa**

**Sequence homology domain 4: 66.6% identity in 9 aa**

**Sequence homology domain 5: 22.3% identity in 112 aa**

**Sequence homology domain 6: 43.8% identity in 16 aa**

```

                                1080
LGS      NPKMKVAGGPNPGPPGF
          .. :. :.:.: :.
BCL9     DAALCKPGGPGGPDFSF
          1190          1200

```

## Figure 8

A

ATGCATTCCAGTAACCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA  
GAGTAGCCCTAAGTCAAAGCAGGAGGTGATGGTCCGTCCCCCTACAGTGA  
TGTCGCCATCTGGAAACCCCCAGCTGGATTCCAAATTCCTCCAATCAGGGT  
AAACAGGGGGGCTCAGCCAGCCAATCCCAGCCATCCCCCTGTGACTCCAA  
GAGTGGGGGGCCATAACCCCTAAAGCACTCCCTGGCCCAGGTGGGAGCATGG  
GGCTGAAGAATGGGGCTGGAAATGGTGCCAAGGGCAAGGGGAAAAGGGAG  
CGAAGTATTTCCGCGCACTCCTTTGATCAGAGAGATCCTGGGACTCCAAA  
CGATGACTCTGACATTAAAGAATGTAATTCTGCTGACCACATAAAGTCCC  
AGGATTCCCAGCACACACCACACTCGATGACCCCATCAAATGCTACAGCC  
CCCAGGTCTTCTACCCCCCTCCCATGGCCAACTACTGCCACAGAGCCAC  
ACCTGCTCAGAAGACTCCAGCCAAAGTGGTGTACGTGTTTTCTACTGAGA  
TGGCCAATAAAGCTGCAGAAGCTGTTTTGAAGGGCCAGGTTGAAACTATC  
GTCTCTTTCCACATCCAGAACATTTCTAACAACAAGACAGAGAGAAGCAC  
AGCGCCTCTGAACACACAGATATCTGCCCTTCGGAATGATCCGAAACCTC  
TCCCACAACAGCCCCAGCTCCGGCCAACCAGGACCAGAATTCTTCCCAG  
AATACCAGACTGCAGCCAACTOCACCCATTCCGGCACCAGCACCCAAAGCC  
TGCGGCACCCCCAAGTCCCTGGACCGGGAGAGTCTGGGGTAGAAAACA  
AACTGATTCTTCTGTAGGAAGTCTGCCAGCTCCTCCTCCTGCCCCCA  
GATGGTACTGGGCCCCAACTCAACTCCCAACAATAGGGCAGTGACCCCTGT  
CTCCAGGGGAGCAATAGCTCTTCAGCAGATCCCAAAGCCCCCTCCGCTC  
CACCAGTGTCCAGTGGCGAGCCCCCAGCACTGGGAGAGAATCCCGATGGC  
CTATCTCAGGAGCAGCTGGAGCACCGGGAGCGCTCCTTACAAACTCTCAG  
AGATATCCAGCGCATGCTTTTTCTGATGAGAAAGAATTACAGGAGCAC  
AAAGTGGGGGACCGCAGCAGAATCCTGGGGTATTAGATGGGCCTCAGAAA  
AAACCAGAAGGGCCAATACAGGCCATGATGGCCCAATCCCAAAGCCTAGG  
TAAGGGACCTGGGCCCCGGACAGACGTGGGAGCTCCATTTGGCCCTCAAG  
GACATAGAGATGTACCCTTTCTCCAGATGAAATGGTTCCACCTTCTATG  
AACTCCAGTCTGGGACCATAGGACCCGACCACCTTGACCATATGACTCC  
CGAGCAGATAGCGTGGCTGAAACTGCAGCAGGAGTTTTATGAAGAGAAGA  
GGAGGAAGCAGGAACAAGTGGTTGTCCAGCAGTGTCCCTCCAGGACATG  
ATGGTCCATCAGCACGGGCCCTCGGGGAGTGGTCCGAGGACCCCCCCTCC  
ATACCAGATGACCCCTAGTGAAGGCTGGGCACTGGGGGTACAGAGCCAT  
TTTCTGATGGTATCAACATGCCACATTCTCTGCCCCGAGGGGCATGGCT  
CCCCACCCCAACATGCCAGGGAGCCAGATGCGCCTCCCTGGATTTGCAGG  
CATGATAAACTCTGAAATGGAAGGGCCGAATGTCCCAACCCCTGCATCTA  
GACCAGGTCTTTCTGGAGTCAGTTGGCCAGATGATGTGCCAAAAATCCGA  
GATGGTCCGAAATTTTCTCCTGGCCAGGGCATTTCAGCGGTCTGGCCG  
AGGGGAACGCTTCCCAAACCCCCAAGGATTGTCTGAAGAGATGTTTCAGC  
AGCAGCTGGCAGAGAAACAGCTGGGTCTCCCCCAGGGATGGCCATGGAA  
GGCATCAGGOCAGCATGGAGATGAACAGGATGATTCCAGGCTCCAGOG  
CCACATGGAGCCTGGGAATAACCCCATTTTCCCTCGAATACCAGTTGAGG  
GCCCTCTGAGTCCTTCTAGGGGTGACTTTCCAAAAGGAATTCCCCCACAG

09454\_072701

Figure 8A

ATGGGCOCTGGTCGGGAACCTTGAGTTTGGGATGGTTCTAGTGGGATGAA  
GGGAGATGTCAATCTAAATGTCAACATGGGATCCAACCTCTCAGATGATAC  
CTCAGAAGATGAGAGAGGCTGGGGCGGGCOCTGAGGAGATGCTGAAATTA  
CGCCCAGGTGGCTCAGACATGCTGCCTGCTCAGCAGAAGATGGTGCCACT  
GCCATTTGGTGAGCACCCCCAGCAGGAGTATGGCATGGGCCCCAGACCAT  
TCCTTCCCATGTCTCAGGGTCCAGGCAGCAACAGTGGCTTGCGGAATCTC  
AGAGAACCAATTGGGCCCCGACCAGAGGACTAACAGCCGGCTCAGTCATAT  
GCCACCACTACCTCTCAACCTTCCAGTAACCCCCACCAGCCTCAACACAG  
CTCCTCCAGTTCAGCGCGGCTGGGGCGGAAGCCCTTGATATATCTGTG  
GCAGGCAGCCAGGTGCATTOCCCAGGCATTAACCCCTCTGAAGTCTCCCAC  
GATGCAOCCAAGTCCAGTCACCAATGCTGGGCTCGCCCTGGGGAAOCTCA  
AGTCCCCCAGACTOCATGCGAGCTGGCAGGCATGCTGGCGGGGCCAGCT  
GCTGCTGCTTCCATTAAAGTCCCCCOCTGTTTTGGGGTCTGCTGCTGCTT  
ACCTGTCCACCTCAAGTCTCCATCACTTCTGCCCCGTCACTGGATGGA  
CCTCTTCTCCAAAACCTCCCCCTTCAGAGTCCCTGGGATCCCTCCAAACCAT  
AAAGCACCCCTCACCATGGCCTCCCCAGCCATGCTGGGAAATGTAGAGTC  
AGGTGGCCCCCACCCTCCTACAGCCAGCCAGCCTGCCTCTGTGAATATCC  
CTGGAAGTCTTCCCTCTAGTACACCTTATACCATGCCTCCAGAGCCAACC  
CTTTCCAGAAACCCACTCTCTATTATGATGTCTCGAATGTCCAAGTTTGC  
AATGCCCAGTTCCACCCCGTTATACCATGATGCTATCAAGACTGTGGCCA  
GCTCAGATGACGACTCCCCCTCAGCTCGTTCTCCCACTTGCCATCAATG  
AATAATATGCCAGGAATGGGCATTAATACACAGAATCCTCGAATTTCAGG  
TCCAAACCCCGTGGTTCCGATGCCAACCCCTCAGCCCCAATGGGAATGACCC  
AGCCACTTTCTCACTCCAATCAGATGCCCTCTCCAAATGCCGTGGGAOCC  
AACATACCTCCTCATGGGGTCCCAATGGGGCCTGGCTTGATGTACACAA  
TCCTATCATGGGGCATGGGTCCCAGGAGCCACCGATGGTACCTCAAGGAC  
GGATGGGCTTCCCCCAGGGCTTCCCTCCAGTACAGTCTCCCCCAGCAG  
GTTCCATTCCCTCACAATGGCCCCAGTGGGGGGCAGGGCAGCTTCCCAGG  
AGGGATGGGTTTCCAGGAGAAGGCCOCCCTTGCCCGCCCCAGCAACCTGC  
CCCAAAGTTCCAGCAGATGCAGCACTTTGCAAGCCTGGAGGCCCGGGGGT  
CCTGACTCCTTCACTGTCCTGGGGAACAGCATGCCTTCGGTGTTTACAGA  
CCCAGATCTGCAGGAGGTATCCGAOCTGGAGCCACCGGAATACCTGAGT  
TTGATCTATCCCGCATTATTCCATCTGAGAAGCCCAGCCAGACGCTGCAA  
TATTTCCCTCGAGGGGAAGTTCCAGGCCGTAAACAGCCCCAGGGTCTGG  
ACCTGGGTTTTACACATGCAGGGGATGATGGGCGAACAAGCCCCAGAA  
TGGGACTAGCATTACCTGGCATGGGAGGTCCAGGGCCAGTGGGAACCTCCG  
GACATCCCTCTTGGTACAGCTCCATCCATGCCAGGCCACAACCCCATGAG  
ACCAACAGCCTTTCTCCAACAAGGCATGATGGGACCTCACCATCGGATGA  
TGTCACCAGCACAATCTACAATGCCCGGCCAGCCACCCCTGATGAGCAAT  
CCAGCTGCTGCGGTGGGCATGATTCTGGCAAGGATCGGGGGCTGCGGG  
GCTCTACACCCACCCCTGGGCTGTGGGCTCTCCAGGCATGATGATGTCCA  
TGCAGGGCATGATGGGACCCCAACAGAACATCATGATCCCCCAGAGATG  
AGGCCCCGGGGCATGGCTGCTGAOGTGGGCATGGGTGGATTTAGCCAAGG  
ACCTGGCAACCCAGGAAACATGATGTTTTAA

0954-0220-EST-60

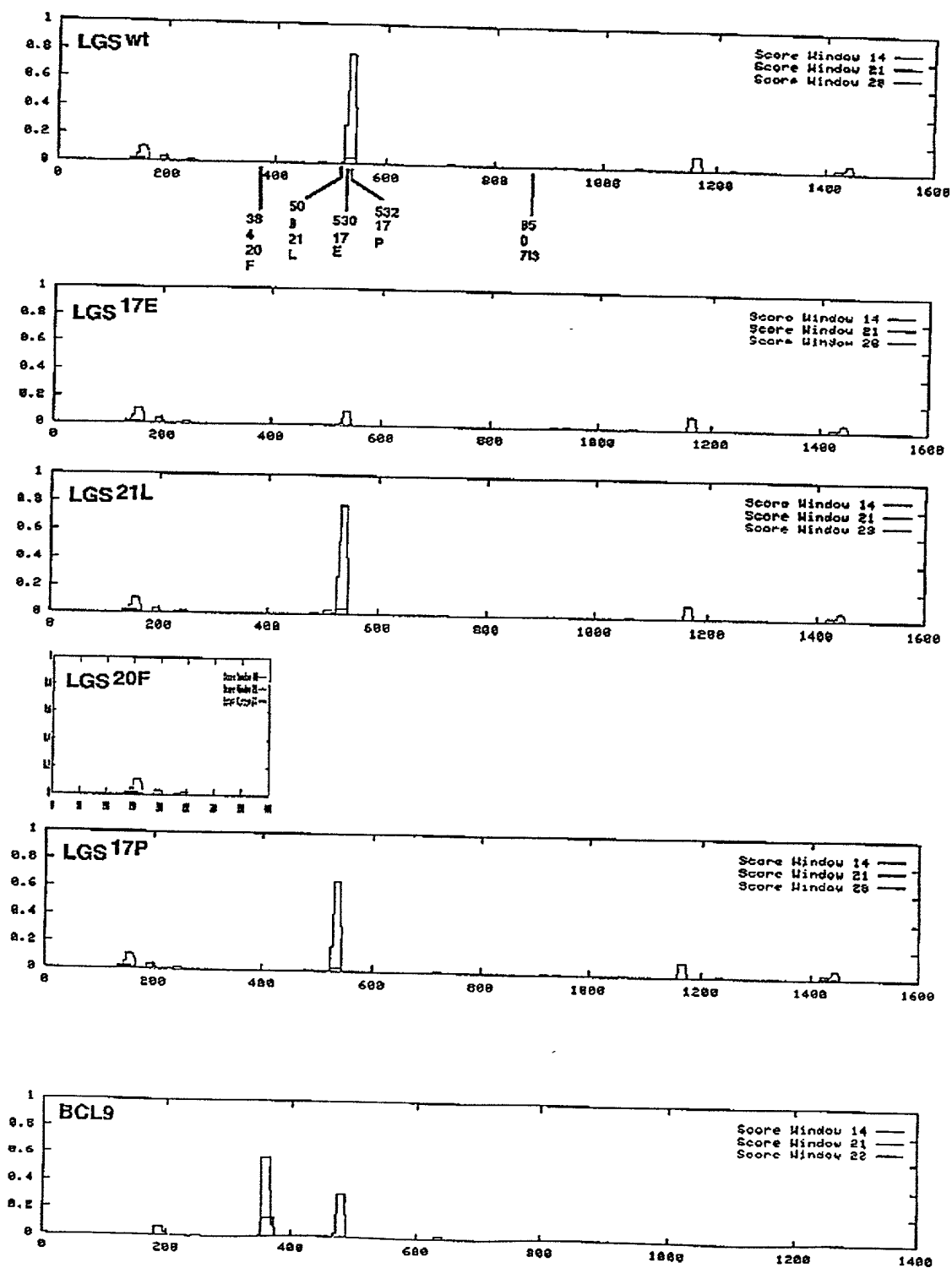
Figure 8B

B

MHSSNPKVRSSPSGNTQSSPKSKQEVMMRPPTVMSPSGNPQLDSKFSNQG  
KQGGASQSQSPSPCDKSGGHTPKALPGPGGSMGLKNGAGNGAKGKGKRE  
RSISADSFDQRDPGTPNDDSDIKECNSADHIKSQDSQHTPHSMTPSNATA  
PRSSTPSHGQTTATEPTPAQKTPAKVVVFSTEMANKAAEAVLKGQVETI  
VSFHQINISNNKTERSTAPLNTQISALRNDPKPLPQQPPAPANQDQNSSQ  
NTRLQPTTPIAPAPKPAAPPRPLDRESPGVENKLIPSVGSPASSTPLPP  
DGTGPNSTPNINRAVTPVSQGSNSSSADPKAPPPPPVSSGEPPTLGENPDG  
LSQEQLHHRERSLQTLRDIQRMILFPDEKEFTGAQSGGPQQNPGVLDGPQK  
KPEGPIQAMMAQSQSLGKGPGPRTDVGAPFGPGQHRDVPFSPDEM/PPSM  
NSQSGTIGPDHLDHMTPEQIAWLKLQQEFYEEKRRKQEQVVVQQCSLQDM  
MVHQHGPRGVVRGPPPPYQMTPEGWAPGGTEPFSDGINMPSLPPRGMA  
PHPNMPGSGMRLPGFAGMINSEMEGPNV/NPASRPGLSGVSWPDDVPKIP  
DGRNFPFGQGIFSGPGRGERFPNPQGLSEEMFQQQLAEKQLGLPPGMAME  
GIRPSMEVNRMPGSGQRHIMEPGNNPIFPRIPEGLSPSRGDFPKGIPPQ  
MGPGRELEFGMVPSGMKGDVNLNVNMGSSNSQMIPQKIMREAGAGPEEMLKL  
RPGGSDMLPAQQKMVPLPFGHEPQQEYGMGPRPFLPMSQGPGSNSGLRNL  
REPIGPDQRTNSRLSHMPPLPLNPSSNPTSLNTAPPVQRGLGRKPLDISV  
AGSQVHSPGINPLKSPTMHQVQSPMLGSPSGNLKSPQTPSQLAGMLAGPA  
AAASIKSPPVLGSAASPVLKSPSLPAPSPGWTSSPKPPLQSPGIPPNH  
KAPLTMASPAMLGNVESGGPPPTASQPASVNIPGSLPSSSTPYTMPPEPT  
LSQNPLSIMMSRMSKFAMPSSTPLYHDAIKTVASSDDDSPPARSPNLPSM  
NNMPGMGINTQNPRISGPNPVVPMPTLSPMGMTOPLSHSNQMPSPNAVGP  
NIPFHGVPMGPGLMSHNPIMGHGSOEPPMVPOGRMGFFPQGFFPVQSPFQQ  
VPFFHNGPSGGQGSFPFGMGFFPGEGLGRPSNLQSSADAALCKPGGPGG  
PDSFTVLGNSMPSVFTDPLQEVIRPGATGIPEFDLSRIIPSEKPSQTLQ  
YFPRGEVPGRKQPGPGPGFSHMQGMGEOAPPIMGLALPGMGPGPVGTP  
DIPLGTAPSMPGHNPMRPPAFLQQGMMGPHHRMMSPAQSTMPGQPTLMSN  
PAAAVGMIPGKDRGPAGLYTHPGVGSPPGMMMSMQGMMGPOQNNIMIPPQM  
RPRGMAADVGMGGFSQGPNGNPMMF\*

104240"EST653

Figure 9



## Figure 10

A

ATGGCCTGCTTCCCATCCCTGCTGCCATCTCCTGCACCCCTAGGGGCACAGTGGGCATCT  
CGGGAGCTGCTCAGCGGACAGACTAGGGTTACCCCCACCCAGGAGGAGAGAAGCTCCAG  
GGAGCCCCGCGCTGTCCCCGCGGTCAATTGCCCCCTGCCCCAGCCAAGCCAATGCACCCA  
GAAAATAAATTGACCAATCATGGCAAGACAGGGAATGGCGGGGCCAATCTCAGCACCAG  
AATGTGAACCAAGGACCCACCTGCAACGTGGGCTCGAAGGGCGTGGGGGCGGGGAACCAT  
GGGGCCAAGGCCAACCCAGATCTCGCCTAGCAACTCAAGTCTGAAGAACCCCCAGGCAGGG  
GTGCCCCCTTTAGCTCGCTCAAGGGCAAGGTGAAGAGGGACCGGAGTGTGTCTGTGGAC  
TCTGGAGAGCAGCGAGAGGCTGGGACCCCATCCCTGGATTTCAGAGGCCAAAGAGGTGGCG  
CCGCGGAGTAAGCGGCGCTGTGTCTGGAGCGGAAGCAGCCGTACAGTGGGGACGAATGG  
TGCTCTGGACCGGACAGTGAGGAGGACGACAAGCCCATTTGGGGCCACCCACAAGCTGCT  
TTCAAAGAAGACCGCTTTTCAGGACAAGGCATCACACTTCTTCTCCAGCACGTACAGTCTT  
GAAACCTCCAGGAGGAAGCTGCCCCAAGCCCCGAAGGCTTCTTCTTGGGGCAGCAGGGC  
CGAGTCATTTGGAACCTCTCTCGGAGGAGCTCCGTGATCAAGGTGCAGATGCGGCAGGT  
GGGCGGCGCTCAATCATGTCTCAATCGCGACGGTGAATGCGAGTGGCTTGTCAAAGAG  
CAGCTGGAGCATCGGGAACGGTCCCTCCAGACGCTGCGAGACATTGAGCGACTGCTGCTC  
CGCAGCGGAGAGACTGAGCCCTTCTCAAGGGGGCCCCAGGAGGAGCGGCGGGCTGAAG  
AAATATGAGGAACCTTGCAGTCCATGATTTACAGACACAGAGCCTAGGGGGCCCCCG  
CTGGAGCATGAAGTGCTGGGCACCCCCCGGTGGGGACATGGGGCAGCAGATGAACATG  
ATGATACAGAGGCTGGGCCAGGACGCTCACGCTGAGCAGGTGGCTGGCGCAAGCTG  
CAGGAGGAGTACTACGAAGAGAAACGGCGGAAGAGGAACAGATTGGCTGCATGGGAGC  
CGTCTCTGCAGGACATGATGGGCATGGGGGGCATGATGTTGAGGGGGCCCCCGCTCCT  
TACCACAGCAAGCTGGGGATCAGTGGCCACCTGGAATGGGTGCGCAGCTGCGGGGGCCC  
ATGGATGTTCAAGATCCCATGCGCTCCGGGGCGGACCTCCCTTTCTTGGGGCCCGTTTC  
CCAGGCAACCATACATACACGGGTACCTGGGTTTGGGGGCATGCAGAGTATGCCCATGGAG  
GTGCCCATGAATGCCATGCAGAGGCCCGTGAGACAGGCATGGGTGGACCGAAGACTTG  
CCCCATATGGGGGGACCCAGCAATTTGCCAGAACACCATGCCCTACCCAGGTGGGCAG  
GGTGAGGCGGAGCGATTTCATGACTCCCCGGGTCCGTGAGGAGCTGCTGCGGCACAGCTG  
CTGGAGAAGCGGTGATGAGCTGCGACGCGCCCCCTGGGCATGGCAGGCAGTGGCATGGGA  
CAGAGCATGGAGATGGAGCGGATGATGCAGGCGCACCGACAGATGGATCCTGCCATGTTT  
CCCCGGCAGATGGCTGGTGGTGAGGGCCTGGCGGGCACTCCCATGGGCATGGAGTTTGGT  
GGAGGCGGGGGCTCCTGAGCCCTCCCATGGGGCAGTCTGGGCTGAGGGAGTGGACCCA  
CCCATGGGGCCAGGCAACCTCAACATGAACATGAATGTCAACATGAACATGAACATGAAC  
CTGAACGTGCAGATGACCCCGCAGCAGCAGATGCTGATGTCGASAGATGCGGGGCCCT  
GGGGACTTGATGGGGCCCCAGGGCTCAGTCTGAGGAGATGGCCCCGGTTTCGGGCCCCAG  
AACAGCAGTGGCATGGTGCCCTTGCCTTCTGCCAACCCGCCAGGACCTCTCAAGTCGCCC  
CAGGTCTCGGCTCCTCCCTCAGTGTCCGTTACCCCACTGGCTCGCCAGCAGGCTCAAG  
TCTCCTTCCATGGCGGTGCCTTCTCCAGGCTGGGTGCCTCACCCAGACGGCCATGCCC  
AGCCCGGGGGTCTCCAGAACAAAGCAGCCGCTCTCAACATGAACCTTCCACCACCCCTG  
AGCAACATGGAACAGGACCCACACCTTCCAGAACCCCTGTCACTGATGATGACCCAG  
ATGTCCAAGTACGCCATGCCAGCTCCACCCGCTCTACCACAATGCCATCAAGACCATC  
GCCACCTCAGACGACGAGCTGCTGCCCGACCGGCCCTGCTGCCCCCCCCACCAACCCG  
CAGGGCTCCGGGGCAGGTGGCCCCGACTCCCTGAATGCCCTGTGGCCAGTGGCCAGC  
TCCTCCAGATGATGCCCTTCCCCCTCGGCTGCAGCAGCCCCATGGTGCCATGGCCCCC  
ACTGGGGGTGGGGGCGGGGGCTGGCCTGCAGCAGCACTACCCGTACGGCATGGCCCTG  
CCTCCCGAGGACCTGCCAACACAGCCGCCAGGCCCATGCCTCCCCAGCAGCACCTGATG  
GGCAAGCCATGGCTGGGCGCATGGGCGACGCATACCCACCGGTTGTCTCCCTGGGGTG  
GCATCAGTGCTGAACGACCCGAGCTGAGCGAGGTGATCCGGGCCACCCCAACGGGGATC  
CCGAGTTGACTTGTGAGGATCATCCCTCTGAGAAGCCAAGCAGCACCTCCAGTAC  
TTCCCCAAGAGCGAGAACCAGCCCCCAAGGCTCAGCCCCCTAATCTGCATCTCATGAAC  
CTGCAGAACATGATGGCGGAGCAGACTCCCTCTCGGCTCCCAACCTCCAGGCCAGCAG  
GGCGATCGGCGCTGGTGGTGGTGATACCGGGTACCGGGCTATGGCGCCGGCGCAGCGC  
TGCCCTCTGTGCGCCAGACCTTCTTCTGTGGTGCAGGGCAGTTTACAGCCGCAAGCAC  
CAGCGGCAGCTGAAGGAGGCTTTGGAGAGGCTCCTGCCCCAGGTGGAGGCGGGCCGCAAG  
GCCATCCGCGCGCTCAGGTGGAGCGCTATGTGCCGAACAGGAGCGATGCTGCTGGTGC  
CTGTGCTGCGGCTGTGAGGTGCGGGAACACCTGAGCCATGGAACCTGACGGTGTGTAC

091543 "072701

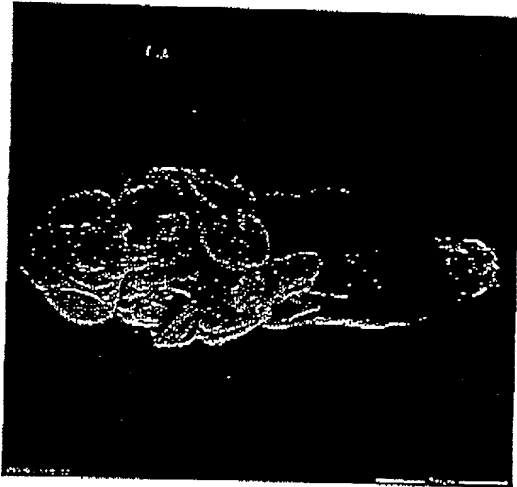


GGGGGGCTGCTGGAGCATCTGGCCAGCCAGAGCACAAAGAAAGCAACCAACAAATTCTGG  
TGGGAGAACAAAGCTGAGGTCCAGATGAAAGAGAAGTTTCTGGTCACTCCCAGGATTAT  
GCGCGATTCAAGAAATCCATGGTGAAAGGTTTGGATTCTATGAGAAAAGGAGGATAAA  
GTGATCAAGGAGATGGCAGCTCAGATCCGTGAGGTGGAGCAGAGCCGACAGGAGGTGGTT  
CGGTCTGTCTTAGAGACAGGTCCCCCAAGATACGCCCTCAGAGTCGGTCCCCCGCGTC  
CTCTCCCGCGCGCAGCTCAAGTCCGGTGCCTTCCCCCGCAGACCCCCGAGGCCACCT  
CAAGCTCGGTGCCTCTGCGCCCCCGCAGGGGCGCCCTCAAGCCTGAGCCCCCGGGCGC  
ACCTCAAGCTCGGTGTACCCCCCATACCCGCAAGGCGCGCCTCATGCCGCGAAG  
ACTTCGCCCCGCCAAGGTGCACCCGTCAAGGCCCGAATAAACCCAGTCACTCCAATT  
GCAGGCAAGACTAGAAAACTGCGCTGCATTGCAACAAAGACTCTTGTGGCGATGAC  
GATACGTGTTTGGGTGTAAACTGTCAATTGCTAATCAGATCTGTGA

FKEDGFQDKASHFFSSYSTSPETSRRLKLPQAPKASFLGQQGRVWVKPLSEE  
LFDQGADAAGGPASIMSPIATVNASGLSKEQLEHRERSLQTLRDIERLLL  
RSGETEPFLKGAPRRSGGLKKYEEPLQSMISQTSLSGGPPLEHEVPGHPP  
GGDMGQQMNMIMIQRLGQDSLTPQVAVWRKLQEEYYEEKRPRKEEQIGLHGS  
RPLQDMGMGMGMVMVRGPPPPYHSKPGDQWPPMGMAQLRGPMDVQDPMQLH  
GGPPFPGRFFGNQIQFVPGFGGQSMPEVPMVPMMAQRPVVRPGMGWTEDL  
PLMGGGSNFAQNTIQRYPVPGGGEAERFMTPRVREELLRHQLLEKSRMGMR  
PLMGAGSGMGQSMEMERMMQAHFRQMDPAMFFPGQMGAGGEGLAGTPMGMEFG  
GGRGLLSPPMGQSGLEVDPPMGPGNLMNMNMNMNMNMNMNLNVQMTPOQQ  
MLMSQKMRGPGDLMGPGQLSPEEMARVRAQNSSGMVPLPSANPPGPLKSP  
QVLGSSLSVRSPTGSPSRLKSPSMAVPSPGWVASPKTAMPSPGVSONKQP  
PLNMNSSTTLNMEQDPTPSQNPLSLMMTQMSKYAMPSSSTPLYHNAIKTI  
ATSDDELLPDRPLPPPPPPQGSFGPGPDSLNPACPGVPFSSSGMMPFPFR  
LQQPHGAMAPTGGGGGGPGLOQGHYPSCMALNAPEDLPNQPPGMPMPQGHLM  
GKQAMAGMGTDAYPPGVLPGVASVLNDPELSEVRPTPTGIPEFDLSRIIP  
SEKPSSTLQYFPKSENQPPKAQPPNLHLMNLQNMMAEQTPSRPPNLPGQQ  
GDRPLVWVPGTRAMAPAQRCLCRQTFFCGRGHVYSRIKHQRQLKEALER  
LLPQVEAARKAIRAAQVERYVPEHERCCWQLCCGCEVREHLSHGNLTVLY  
GGLLEHLASPEHKATNKFWWENKAEVQMKEKFLVTPQDYARFKKSMVKG  
LDSYEKEDKVIKEMAAQIREVEQSRQEVVRSVLETGPPRYALTVRSPAV  
LSRRTLKSGAFPPQTPPEAHPQARCLCAPRRGALKPEPPGRTLKLGVPPHT  
TRKARPHAAKTSPPRPRCTRQAPNKTQSLQLAGKARKTALHLQTKALVGDD  
DTVLGVKLSIANYDL

Figure 11

A



B



20220" CHS 650

Figure 12

A

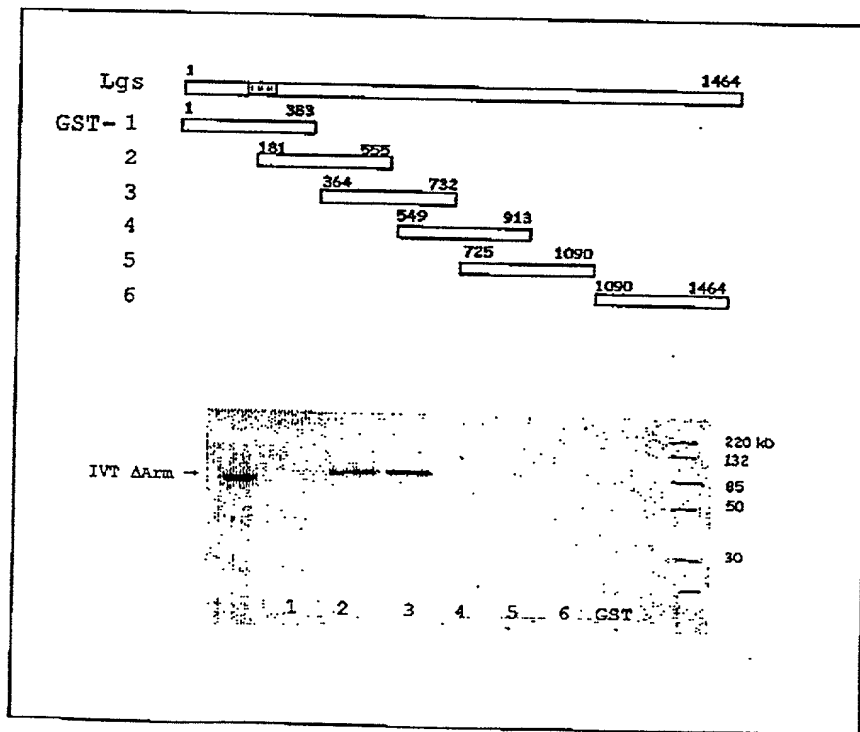
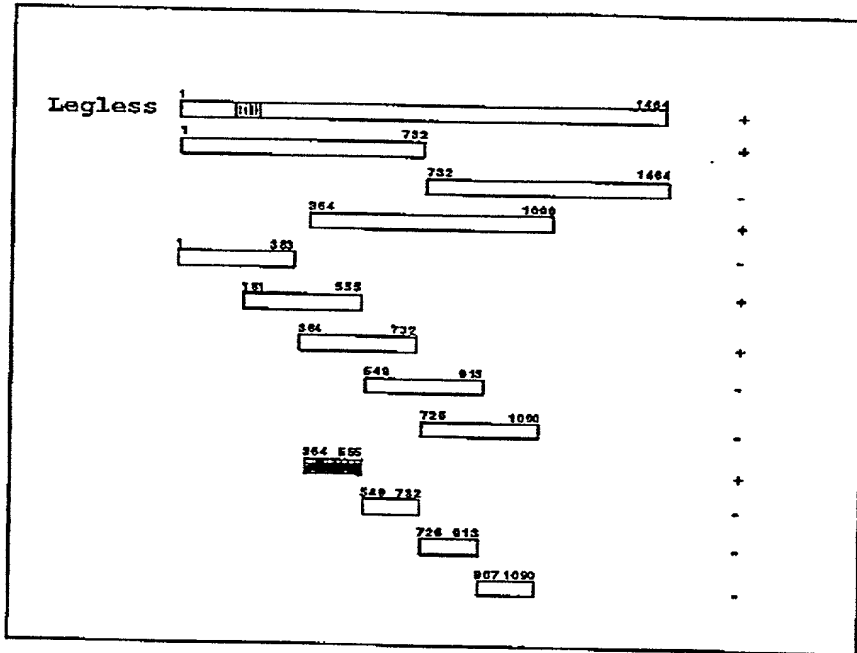


Figure 12B

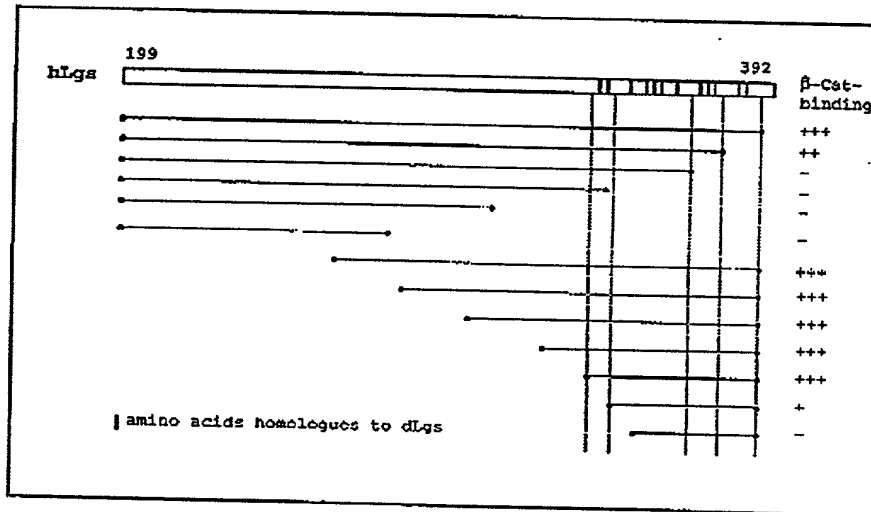
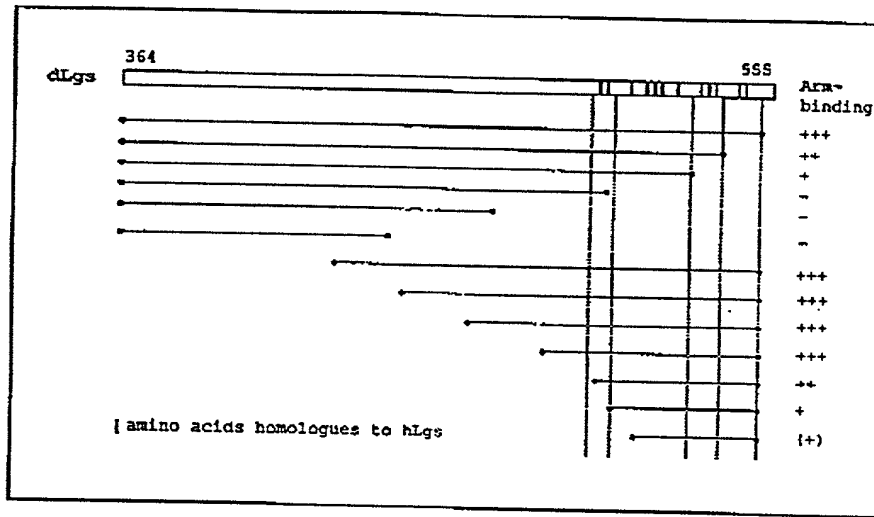


Figure 12C










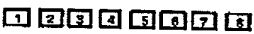

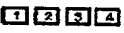




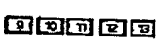
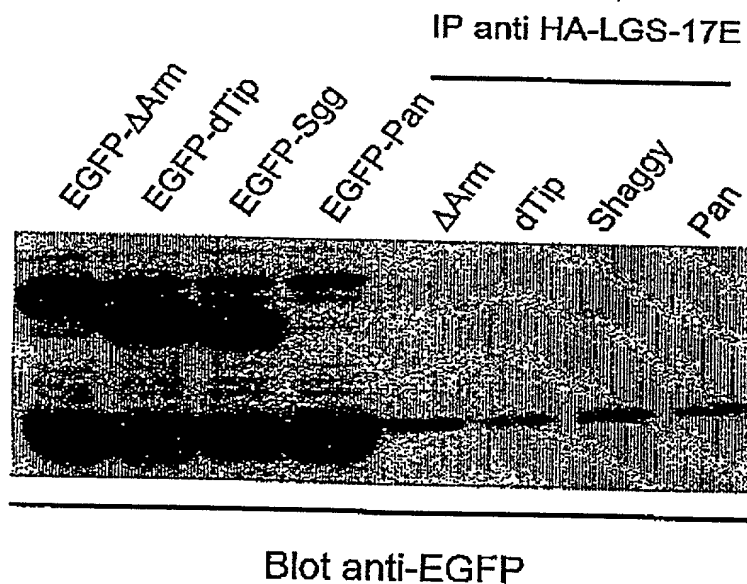
	In vitro interaction
N  C	++
 C	++
 C	-
N  C	++
N  C	+++
N  C	+++
N  C	++
N  C	-
 C	++
 C	+++
 C	+++
 C	++
 C	-
 C	(+)
 C	(-)
 C	(-)
 C	(-)

Figure 13

A



B

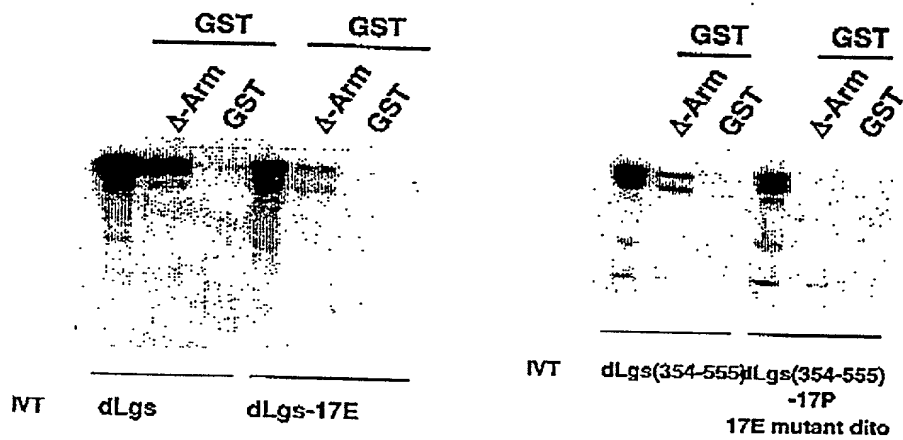
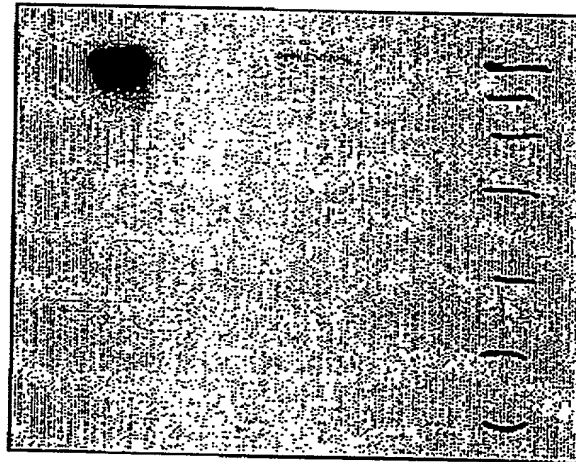


Figure 13

C

IVT	GST	GST-
input		$\beta$ -Cat

IVT-hLgs →



D

IVT input	GST	GST- β-Cat
--------------	-----	---------------

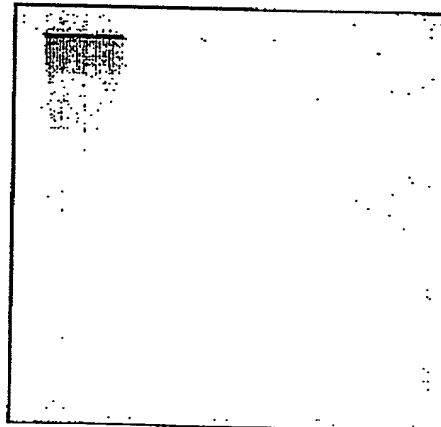
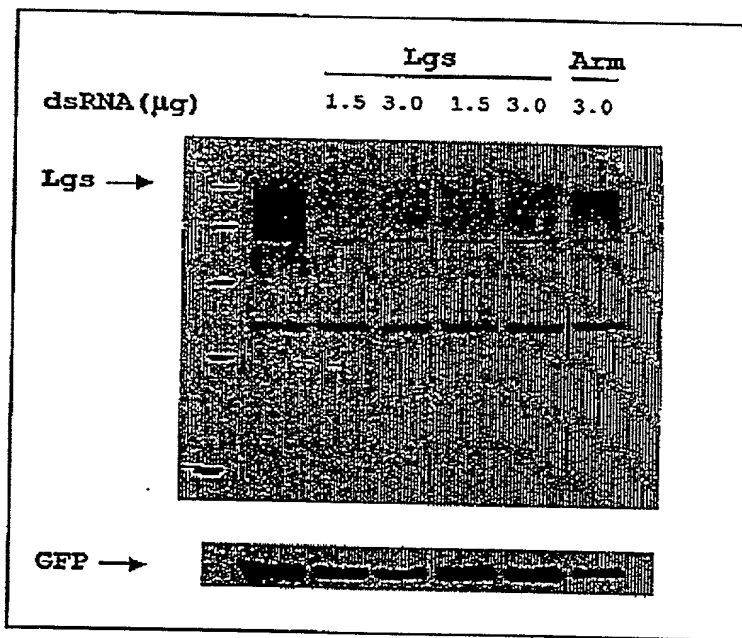
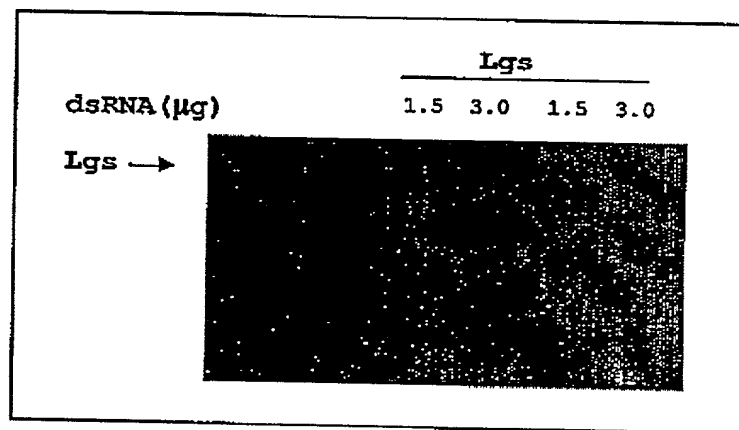
IVT-hLgscdn  $\rightarrow$ [illegible]

Figure 14



pMT-EGFP (μg)    1.5   1.5   1.5   1.5   1.5   1.5

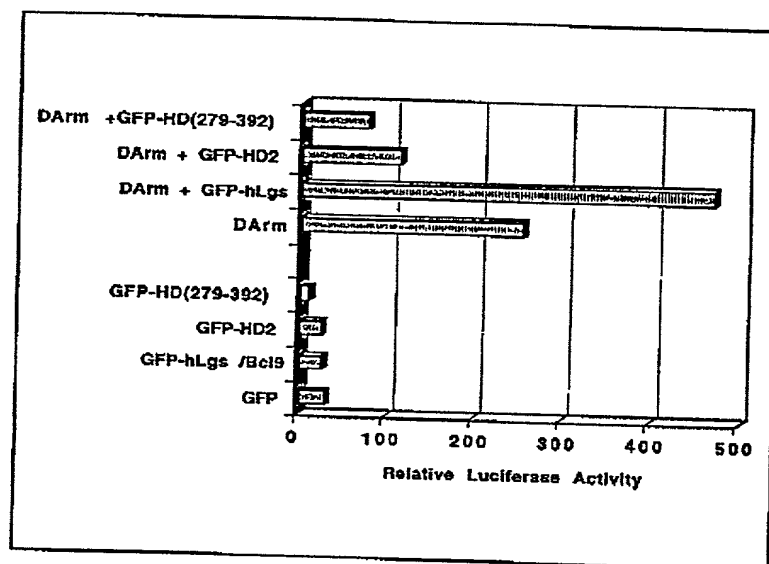


pMT-dLgs (μg)    -    2    2    2    2    2



Figure 15

A



B

